

i) Applicant: ISRAEL David and Wolfman, Neil M.

(ii) TITLE OF INVENTION: RECOMBINANT BONE MORPHOGENETIC PROTEIN HETERODIMERS, COMPOSITIONS AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

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- (E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/864,692
- (B) FILING DATE: 07-APR-1992
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kapinos, Ellen J.
- (B) REGISTRATION NUMBER: 32,245
- (C) REFERENCE/DOCKET NUMBER: GI-5192A

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 356..1543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACCTG CAGGGAGAAT	60
AACTTGCGCA CCCCACTTG CGCCGGTGCC TTTGCCCGAG CGGAGCCTGC TTGCCCATCT	120
CCGAGCCCCA CCGCCCCCTCC ACTCCTCGGC CTTGCCCGAC ACTGAGACGC TGTCCCCAGC	180

GTTGAAAGAG AGACTGCGCG GCCGGCACCGGGAGAAGGA GGAGGCAAAG AAAAGGAAC	240
GACATTGGGT CCTTGCGCCA GGTCTTTGA CCAGAGTTT TCCATGTGGA CGCTCTTCA	300
ATGGACGTGT CCCCGCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG Met 1	358
GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu 5 10 15	406
CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe 20 25 30	454
GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val 35 40 45	502
CTG AGC GAG TTC GAG TTG CCG CTG CTC AGC ATG TTC GGC CTG AAA CAG Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln 50 55 60 65	550
AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp 70 75 80	598
CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His 85 90 95	646
CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His 100 105 110	694
CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACC AGT GGG AAA ACA ACC His Glu Glu Ser Leu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr 115 120 125	742
CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC Arg Arg Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile 130 135 140 145	790
ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT TTA Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu 150 155 160	838
GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile 165 170 175	886
AAA CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp 180 185 190	934
ACC AGG TTG GTG AAT CAG AAT GCA AGC AGG TGG GAA ACT TTT GAT GTC Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp Val 195 200 205	982

ACC CCC GCT GTG ATG CGG TGG ACT CA CAG GGA CAC GCC AAC CAT GGA		1030
Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His Gly		
210 215 220 225		
TTC GTG GTG GAA GTG GCC CAC TTG GAG GAG AAA CAA GGT GTC TCC AAG		1078
Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser Lys		
230 235 240		
AGA CAT GTT AGG ATA AGC AGG TCT TTG CAC CAA GAT GAA CAC AGC TGG		1126
Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser Trp		
245 250 255		
TCA CAG ATA AGG CCA TTG CTA GTA ACT TTT GGC CAT GAT GGA AAA GGG		1174
Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys Gly		
260 265 270		
CAT CCT CTC CAC AAA AGA GAA AAA CGT CAA GCC AAA CAC AAA CAG CGG		1222
His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg		
275 280 285		
AAA CGC CTT AAG TCC AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC		1270
Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe		
290 295 300 305		
AGT GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC		1318
Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His		
310 315 320		
GCC TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG		1366
Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu		
325 330 335		
AAC TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC		1414
Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn		
340 345 350		
TCT AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC		1462
Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile		
355 360 365		
TCG ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT		1510
Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr		
370 375 380 385		
CAG GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA		1563
Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg		
390 395		
CATAAAATATA TATATATATA TATATTTAG AAAAAAGAAA AAAA		1607

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION SEQ ID NO:2:

Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Pro Gln Val
 1 5 10 15

Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
 20 25 30

Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
 35 40 45

Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
 50 55 60

Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
 65 70 75 80

Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
 85 90 95

His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
 100 105 110

His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
 115 120 125

Thr Arg Arg Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
 130 135 140

Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
 145 150 155 160

Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
 165 170 175

Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
 180 185 190

Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp
 195 200 205

Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
 210 215 220

Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
 225 230 235 240

Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
 245 250 255

Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
 260 265 270

Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
 275 280 285

Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
 290 295 300

Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr

305 310 315 320

His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
325 330 335

Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
340 345 350

Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
355 360 365

Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn
370 375 380

Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
385 390 395

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1954 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 403..1626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA 60

GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG 120

AGTATCTAGC TTGTCTCCCC GATGGGATTG CCGTCCAAGC TATCTCGAGC CTGCAGCGCC 180

ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG 240

CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC 300

GCACTGCTGC AGCTTCCCTG AGCCTTCCA GCAAGTTGT TCAAGATTGG CTGTCAAGAA 360

TCATGGACTG TTATTATATG CCTTGTTTTC TGTCAAGACA CC ATG ATT CCT GGT 414
Met Ile Pro Gly
1

AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC 462
Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly
5 10 15 20

GCG AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC 510
Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala
25 30 35

GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG 558

Glu Ile Gln Gly His Ala Gly Gly	Arg Arg Ser Gly Gln Ser His Glu	
40	45	50
CTC CTG CGG GAC TTC GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC		606
Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met Phe Gly Leu Arg		
55	60	65
CGC CGC CCG CAG CCT AGC AAG AGT GCC GTC ATT CCG GAC TAC ATG CGG		654
Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro Asp Tyr Met Arg		
70	75	80
GAT CTT TAC CGG CTT CAG TCT GGG GAG GAG GAG GAA GAG CAG ATC CAC		702
Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Gln Ile His		
85	90	95
100		
AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC AGC CGG GCC AAC ACC		750
Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser Arg Ala Asn Thr		
105	110	115
GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC CCA GGG ACC		798
Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile Pro Gly Thr		
120	125	130
AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC CCT		846
Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile Pro		
135	140	145
GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG		894
Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln		
150	155	160
GTG GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT		942
Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile		
165	170	175
180		
TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC		990
Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile		
185	190	195
ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG		1038
Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp		
200	205	210
GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG		1086
Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys		
215	220	225
CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT		1134
Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr		
230	235	240
CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA		1182
Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln		
245	250	255
260		
GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC		1230
Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly		
265	270	275
CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG CGT		1278

His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys Arg		
280	285	290
AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC		1326
Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys		
295	300	305
CGG CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC		1374
Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp		
310	315	320
TGG ATT GTG GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC		1422
Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp		
325	330	340
TGC CCC TTT CCA CTG GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT		1470
Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile		
345	350	355
GTG CAG ACC CTG GTC AAT TCT GTC AAT TCC AGT ATC CCC AAA GCC TGT		1518
Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys		
360	365	370
TGT GTG CCC ACT GAA CTG ACT GCC ATC TCC ATG CTG TAC CTG GAT GAG		1566
Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu		
375	380	385
TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG ATG GTA GTA GAG GGA		1614
Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly		
390	395	400
TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG ATATACACAC		1666
Cys Gly Cys Arg		
405		
CACACACACA CACCACATAC ACCACACACA CACGTTCCCCA TCCACTCACC CACACACTAC		1726
ACAGACTGCT TCCTTATAGC TGGACTTTA TTTAAAAAAA AAAAAAAA AATGGAAAAA		1786
ATCCCTAAC ATTCAACCTTG ACCTTATTAG TGACTTTAGG TGCAAATGTT TTGACCATAT		1846
TGATCATATA TTTGACAAA ATATATTAT AACTACGTAT TAAAAGAAAA AAATAAAATG		1906
AGTCATTATT TTAAAAAAA AAAAAAAACT CTAGACTCGA CGGAATTG		1954

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val			
1	5	10	15

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
20 25 30

Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
35 40 45

Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
50 55 60

Phe Gly Leu Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
65 70 75 80

Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu
85 90 95

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
100 105 110

Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
115 120 125

Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
130 135 140

Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu
145 150 155 160

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
165 170 175

Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
180 185 190

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
195 200 205

Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
210 215 220

Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
225 230 235 240

Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
245 250 255

Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
260 265 270

Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
275 280 285

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
290 295 300

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
305 310 315 320

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
325 330 335

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
340 345 350

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
355 360 365

Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
370 375 380

Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
385 390 395 400

Val Val Glu Gly Cys Gly Cys Arg
405

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGACCGAGC GGCGCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG TGCGGGGCCG 60

GAGCCCGGAG CCCGGGTAGC GCGTAGAGCC GGCGCG ATG CAC GTG CGC TCA CTG 114
Met His Val Arg Ser Leu
1 5

CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA CCC CTG TTC 162
Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro Leu Phe
10 15 20

CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC GAG GTG CAC 210
Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu Val His
25 30 35

TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG GAG ATG 258
Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg Glu Met
40 45 50

CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC CCG CGC CCG 306
Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro
55 60 65 70

CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG 354
His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu
75 80 85

TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC 402

Tyr Asn Ala Met Ala Val Glu Glu	Sly Gly Gly Pro Gly Gly Gln Gly		
90	95	100	
TTC TCC TAC CCC TAC AAG GCC GTC	TTC AGT ACC CAG GGC CCC CCT CTG		450
Phe Ser Tyr Pro Tyr Lys Ala Val	Phe Ser Thr Gln Gly Pro Pro Leu		
105	110	115	
GCC AGC CTG CAA GAT AGC CAT	TTC CTC ACC GAC GCC GAC ATG GTC ATG		498
Ala Ser Leu Gln Asp Ser His Phe	Leu Thr Asp Ala Asp Met Val Met		
120	125	130	
AGC TTC GTC AAC CTC GTG GAA CAT	GAC AAG GAA TTC TTC CAC CCA CGC		546
Ser Phe Val Asn Leu Val Glu His	Asp Lys Glu Phe Phe His Pro Arg		
135	140	145	150
TAC CAC CAT CGA GAG TTC CGG TTT	GAT CTT TCC AAG ATC CCA GAA GGG		594
Tyr His His Arg Glu Phe Arg Phe	Asp Leu Ser Lys Ile Pro Glu Gly		
155	160	165	
GAA GCT GTC ACG GCA GCC GAA	TTC CCG ATC TAC AAG GAC TAC ATC CGG		642
Glu Ala Val Thr Ala Ala Glu Phe	Arg Ile Tyr Lys Asp Tyr Ile Arg		
170	175	180	
GAA CGC TTC GAC AAT GAG ACG	TTC CCG ATC AGC GTT TAT CAG GTG CTC		690
Glu Arg Phe Asp Asn Glu Thr Phe	Arg Ile Ser Val Tyr Gln Val Leu		
185	190	195	
CAG GAG CAC TTG GGC AGG GAA	TCG GAT CTC TTC CTG CTC GAC AGC CGT		738
Gln Glu His Leu Gly Arg Glu Ser	Asp Leu Phe Leu Leu Asp Ser Arg		
200	205	210	
ACC CTC TGG GCC TCG GAG GGC	TGG CTG GTG TTT GAC ATC ACA GCC		786
Thr Leu Trp Ala Ser Glu Glu	Gly Trp Leu Val Phe Asp Ile Thr Ala		
215	220	225	230
ACC AGC AAC CAC TGG GTG GTC	AAT CCG CGG CAC AAC CTG GGC CTG CAG		834
Thr Ser Asn His Trp Val Val	Asn Pro Arg His Asn Leu Gly Leu Gln		
235	240	245	
CTC TCG GTG GAG ACG CTG GAT	GGG CAG AGC ATC AAC CCC AAG TTG GCG		882
Leu Ser Val Glu Thr Leu Asp	Gly Gln Ser Ile Asn Pro Lys Leu Ala		
250	255	260	
GGC CTG ATT GGG CGG CAC GGG	CCC CAG AAC AAG CAG CCC TTC ATG GTG		930
Gly Leu Ile Gly Arg His Gly	Pro Gln Asn Lys Gln Pro Phe Met Val		
265	270	275	
GCT TTC TTC AAG GCC ACG GAG	GTC CAC TTC CGC AGC ATC CGG TCC ACG		978
Ala Phe Phe Lys Ala Thr Glu	Val His Phe Arg Ser Ile Arg Ser Thr		
280	285	290	
GGG AGC AAA CAG CGC AGC CAG	AAC CGC TCC AAG ACG CCC AAG AAC CAG		1026
Gly Ser Lys Gln Arg Ser Gln	Asn Arg Ser Lys Thr Pro Lys Asn Gln		
295	300	305	310
GAA GCC CTG CGG ATG GCC AAC	GTG GCA GAG AAC AGC AGC AGC GAC CAG		1074
Glu Ala Leu Arg Met Ala Asn	Val Ala Glu Asn Ser Ser Ser Asp Gln		
315	320	325	
AGG CAG GCC TGT AAG AAG CAC	GAG CTG TAT GTC AGC TTC CGA GAC CTG		1122

Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu			
330	335	340	
GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC GCC TAC TAC			1170
Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr			
345	350	355	
TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC ACC			1218
Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr			
360	365	370	
AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG			1266
Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr			
375	380	385	390
GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC GTC			1314
Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val			
395	400	405	
CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA AAC			1362
Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn			
410	415	420	
ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC GAGAATTCA			1409
Met Val Val Arg Ala Cys Gly Cys His			
425	430		
ACCCTTGGG GCCAAGTTT TCTGGATCCT CCATTGCTC			1448

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala			
1	5	10	15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser			
20	25	30	
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser			
35	40	45	
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu			
50	55	60	
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro			
65	70	75	80
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly			
85	90	95	
Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser			

100

105

110

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
115 120 125

Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
130 135 140

Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
145 150 155 160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
165 170 175

Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
195 200 205

Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
225 230 235 240

His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
260 265 270

Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
275 280 285

Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
290 295 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
305 310 315 320

Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
325 330 335

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
340 345 350

Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Human placenta

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Stratagene catalog #936203 Human placenta
cDNA library
- (B) CLONE: BMP6C35

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 160..1701

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1282..1698

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 1..2923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC GAGAGGTGGC	60
GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG GCCTCGCTCC GCCGCTCCAC	120
GCCTCGCGGG ATCCGCGGGG GCAGCCCCGGC CGGGCGGGG ATG CCG GGG CTG GGG Met Pro Gly Leu Gly -374 -370	174
CGG AGG GCG CAG TGG CTG TGC TGG TGG GGG CTG CTG TGC AGC TGC Arg Arg Ala Gln Trp Leu Cys Trp Trp Gly Leu Leu Cys Ser Cys -365 -360 -355	222
TGC GGG CCC CCG CCG CTG CGG CCC TTG CCC GCT GCC GCG GCC Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro Ala Ala Ala Ala -350 -345 -340	270
GCC GCC GGG GGG CAG CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr -335 -330 -325	318

GAG CAG CCG CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg -320 -315 -310	366
CGG CTC AAG ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln Lys Glu Ile Leu Ser -305 -300 -295 -290	414
GTG CTG GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln -285 -280 -275	462
CCG CAG CCC CCG GCG CTC CGG CAG CAG GAG GAG CAG CAG CAG CAG CAG Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln -270 -265 -260	510
CAG CTG CCT CGC GGA GAG CCC CCT CCC GGG CGA CTG AAG TCC GCG CCC Gln Leu Pro Arg Gly Glu Pro Pro Gly Arg Leu Lys Ser Ala Pro -255 -250 -245	558
CTC TTC ATG CTG GAT CTG TAC AAC GCC CTG TCC GCC GAC AAC GAC GAG Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn Asp Glu -240 -235 -230	606
GAC GGG GCG TCG GAG GGG GAG AGG CAG CAG TCC TGG CCC CAC GAA GCA Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro His Glu Ala -225 -220 -215 -210	654
GCC AGC TCG TCC CAG CGT CGG CAG CCG CCC CCG GGC GCC GCG CAC CCG Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro Gly Ala Ala His Pro -205 -200 -195	702
CTC AAC CGC AAG AGC CTT CTG GCC CCC GGA TCT GGC AGC GGC GGC GCG Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser Gly Ser Gly Gly Ala -190 -185 -180	750
TCC CCA CTG ACC AGC GCG CAG GAC AGC GGC TTC CTC AAC GAC GCG GAC Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe Leu Asn Asp Ala Asp -175 -170 -165	798
ATG GTC ATG AGC TTT GTG AAC CTG GTG GAG TAC GAC AAG GAG TTC TCC Met Val Met Ser Phe Val Asn Leu Val Glu Tyr Asp Lys Glu Phe Ser -160 -155 -150	846
CCT CGT CAG CGA CAC CAC AAA GAG TTC AAG TTC AAC TTA TCC CAG ATT Pro Arg Gln Arg His His Lys Glu Phe Lys Phe Asn Leu Ser Gln Ile -145 -140 -135 -130	894
CCT GAG GGT GAG GTG GTG ACG GCT GCA GAA TTC CGC ATC TAC AAG GAC Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp -125 -120 -115	942
TGT GTT ATG GGG AGT TTT AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr -110 -105 -100	990
CAA GTC TTA CAG GAG CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG Gln Val Leu Gln Glu His Gln His Arg Asp Ser Asp Leu Phe Leu Leu -95 -90 -85	1038

GAC ACC CGT GTA GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp -80 . -75 -70	1086
ATC ACG GCC ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn Met -65 -60 -55 -50	1134
GGG CTT CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro -45 -40 -35	1182
CGA GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro -30 -25 -20	1230
TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC ACC Phe Met Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr Thr -15 -10 -5	1278
AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC TCT ACC Arg Ser Ala Ser Ser Arg Arg Gln Gln Ser Arg Asn Arg Ser Thr 1 5 10 15	1326
CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT TAC AAC AGC Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp Tyr Asn Ser 20 25 30	1374
AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG TAT GTG AGT TTC Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr Val Ser Phe 35 40 45	1422
CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA CCC AAG GGC TAT GCT Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala 50 55 60	1470
GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC CCA CTC AAC GCA CAC ATG Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met 65 70 75	1518
AAT GCA ACC AAC CAC GCG ATT GTG CAG ACC TTG GTT CAC CTT ATG AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Leu Met Asn 80 85 90 95	1566
CCC GAG TAT GTC CCC AAA CCG TGC TGT GCG CCA ACT AAG CTA AAT GCC Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala 100 105 110	1614
ATC TCG GTT CTT TAC TTT GAT GAC AAC TCC AAT GTC ATT CTG AAA AAA Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys 115 120 125	1662
TAC AGG AAT ATG GTT GTA AGA GCT TGT GGA TGC CAC TAACTCGAAA Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 130 135 140	1708
CCAGATGCTG GGGACACACA TTCTGCCTTG GATTCCCTAGA TTACATCTGC CTTAAAAAAA	1768
CACGGAAGCA CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT	1828

TATTACCCAG GAAGATTTA AAGGACCTCA TTAATAATTG GCTCACTTGG TAAATGACGT	1888
GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT GTAGCATAAG GTCTGGTAAC	1948
TGCAGAAACA TAACCGTGAA GCTCTTCCTA CCCTCCTCCC CCAAAAACCC ACCAAAATTA	2008
GTTTAGCTG TAGATCAAGC TATTGGGT GTTTGTTAGT AAATAGGGAA AATAATCTCA	2068
AAGGAGTTAA ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT	2128
AGATTTACA GAGAACAGAA ATCGGGGAAG TGGGGGAAAC GCCTCTGTTC AGTCATTCC	2188
CAGAAGTCCA CAGGACGCAC AGCCCAGGCC ACAGCCAGGG CTCCACGGGG CGCCCTTGTG	2248
TCAGTCATTG CTGTTGTATG TTCGTGCTGG AGTTTGTG GTGTGAAAT ACACTTATT	2308
CAGCCAAAAC ATACCATTTC TACACCTCAA TCCTCCATTG GCTGTACTCT TTGCTAGTAC	2368
CAAAGTAGA CTGATTACAC TGAGGTGAGG CTACAAGGGG TGTGTAACCG TGTAACACGT	2428
GAAGGCAGTG CTCACCTCTT CTTTACCAAGA ACGGTTCTT GACCAGCACA TAAACTCTG	2488
GACTGCCGGC TCTAGTACCT TTTCAGTAAA GTGGTTCTCT GCCTTTTAC TATACAGCAT	2548
ACCACGCCAC AGGGTTAGAA CCAACGAAGA AAATAAAATG AGGGTGCCCA GCTTATAAGA	2608
ATGGTGTAG GGGGATGAGC ATGCTGTTA TGAACGGAAA TCATGATTTC CCTGTAGAAA	2668
GTGAGGCTCA GATTAAATT TAGAATATT TCTAAATGTC TTTTCACAA TCATGTGACT	2728
GGGAAGGCAA TTTCATACTA AACTGATTAA ATAATACATT TATAATCTAC AACTGTTGC	2788
ACTTACAGCT TTTTTGTAA ATATAAACTA TAATTATTG TCTATTTAT ATCTGTTTG	2848
CTGTGGCGTT GGGGGGGGGG CCGGGCTTTT GGGGGGGGGG GTTTGTTGG GGGGTGTCGT	2908
GGTGTGGCG GGGCG	2923

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly
 -374 -370 -365 -360

Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro
 -355 -350 -345

Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly
 -340 -335 -330

Ser Pro Gly Arg Thr Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser
-325 -320 -315

Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln
-310 -305 -300 -295

Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu
-290 -285 -280

His Gly Leu Gln Gln Pro Gln Pro Ala Leu Arg Gln Gln Glu Glu
-275 -270 -265

Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg
-260 -255 -250

Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser
-245 -240 -235

Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser
-230 -225 -220 -215

Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro
-210 -205 -200

Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser
-195 -190 -185

Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe
-180 -175 -170

Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr
-165 -160 -155

Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe
-150 -145 -140 -135

Asn Leu Ser Gln Ile Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe
-130 -125 -120

Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe
-115 -110 -105

Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu His Gln His Arg Asp Ser
-100 -95 -90

Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly
-85 -80 -75

Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr
-70 -65 -60 -55

Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly
-50 -45 -40

Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro
-35 -30 -25

Tyr Asp Lys Gln Pro Phe Met Val Ala Phe Phe Lys Val Ser Glu Val
-20 -15 -10

His Val Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser
-5 1 5 10

Arg Asn Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala
15 20 25

Ser Asp Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu
30 35 40

Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
45 50 55

Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro
60 65 70

Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
75 80 85 90

Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro
95 100 105

Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn
110 115 120

Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys
125 130 135

His

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (H) CELL LINE: U2-OS osteosarcoma

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U2-OS human osteosarcoma cDNA library
- (B) CLONE: U2-16

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 699..2063

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1647..2060

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 1..2153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGTATATT TGTGCCTGCT GGAGGTGGAA TTAACAGTAA GAAGGAGAAA GGGATTGAAT	60
GGACTTACAG GAAGGATTTC AAGTAAATTG AGGGAAACAC ATTTACTTGA ATAGTACAAC	120
CTAGAGTATT ATTTTACACT AAGACGACAC AAAAGATGTT AAAGTTATCA CCAAGCTGCC	180
GGACAGATAT ATATTCCAAC ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC	240
AGGATTGTT TTGGAAAGAG CTCAAGGGTT GAGAAGAACT CAAAAGCAAG TGAAGATTAC	300
TTTGGGAACt ACAGTTTATC AGAAGATCAA CTTTGCTAA TTCAAATACC AAAGGCCTGA	360
TTATCATAAA TTCATATAGG AATGCATAGG TCATCTGATC AAATAATATT AGCCGTCTTC	420
TGCTACATCA ATGCAGCAAA AACTCTAAC AACTGTGGAT AATTGGAAAT CTGAGTTCA	480
GCTTTCTTAG AAATAACTAC TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA	540
TCGGTGAGGA TGTTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTT	600
TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTT AAGAGGACAA	660
GAAGGACTAA AAATATCAAC TTTGCTTTT GGACAAAA ATG CAT CTG ACT GTA Met His Leu Thr Val -316-315	713
TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC TGG AGC TGC TGG GTT CTA Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp Ser Cys Trp Val Leu -310 -305 -300	761
GTG GGT TAT GCA AAA GGA GGT TTG GGA GAC AAT CAT GTT CAC TCC AGT Val Gly Tyr Ala Lys Gly Leu Gly Asp Asn His Val His Ser Ser -295 -290 -285 -280	809
TTT ATT TAT AGA AGA CTA CGG AAC CAC GAA AGA CGG GAA ATA CAA AGG Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg Arg Glu Ile Gln Arg -275 -270 -265	857
GAA ATT CTC TCT ATC TTG GGT TTG CCT CAC AGA CCC AGA CCA TTT TCA Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro Phe Ser -260 -255 -250	905
CCT GGA AAA ATG ACC AAT CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala Pro Leu Phe Met Leu -245 -240 -235	953
GAT CTC TAC AAT GCC GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val -230 -225 -220	1001
AGG GCA TCC TTG GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro -215 -210 -205 -200	1049

GCC TCT CCC AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr -195 -190 -185	1097
CCT CTG ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn -180 -175 -170	1145
TTT CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu -165 -160 -155	1193
AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT CGA Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe Arg -150 -145 -140	1241
TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA GCT GAA Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala Ala Glu -135 -130 -125 -120	1289
TTC CGG ATA TAC AAG GAC CGG AGC AAC CGA TTT GAA AAT GAA ACA Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu Asn Glu Thr -115 -110 -105	1337
ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC ACA AAT AGG GAT Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr Thr Asn Arg Asp -100 -95 -90	1385
GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC CAA GCT TTA GAT GTG Ala Asp Leu Phe Leu Asp Thr Arg Lys Ala Gln Ala Leu Asp Val -85 -80 -75	1433
GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC AGC AAT CAT TGG GTG ATT Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser Asn His Trp Val Ile -70 -65 -60	1481
AAT CCC CAG AAT AAT TTG GGC TTA CAG CTC TGT GCA GAA ACA GGG GAT Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys Ala Glu Thr Gly Asp -55 -50 -45 -40	1529
GGA CGC AGT ATC AAC GTA AAA TCT GCT GGT CTT GTG GGA AGA CAG GGA Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu Val Gly Arg Gln Gly -35 -30 -25	1577
CCT CAG TCA AAA CAA CCA TTC ATG GTG GCC TTC AAG GCG AGT GAG Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Ser Glu -20 -15 -10	1625
GTA CTT CTT CGA TCC GTG AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn -5 1 5	1673
CGC AAT AAA TCC AGC TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT Arg Asn Lys Ser Ser His Gln Asp Ser Ser Arg Met Ser Ser Val 10 15 20 25	1721
GGA GAT TAT AAC ACA AGT GAG CAA AAA CAA GCC TGT AAG AAG CAC GAA Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala Cys Lys Lys His Glu 30 35 40	1769

CTC TAT GTG AGC TTC CGG GAT CTG GGA TGG CAG GAC TGG ATT ATA GCA Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala 45 50 55	1817
CCA GAA GGA TAC GCT GCA TTT TAT TGT GAT GGA GAA TGT TCT TTT CCA Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly Glu Cys Ser Phe Pro 60 65 70	1865
CTT AAC GCC CAT ATG AAT GCC ACC AAC CAC GCT ATA GTT CAG ACT CTG Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu 75 80 85	1913
GTT CAT CTG ATG TTT CCT GAC CAC GTA CCA AAG CCT TGT TGT GCT CCA Val His Leu Met Phe Pro Asp His Val Pro Lys Pro Cys Cys Ala Pro 90 95 100 105	1961
ACC AAA TTA AAT GCC ATC TCT GTT CTG TAC TTT GAT GAC AGC TCC AAT Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn 110 115 120	2009
GTC ATT TTG AAA AAA TAT AGA AAT ATG GTA GTA CGC TCA TGT GGC TGC Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ser Cys Gly Cys 125 130 135	2057
CAC TAATATTAAA TAATATTGAT AATAACAAAA AGATCTGTAT TAAGGTTTAT His	2110
GGCTGCAATA AAAAGCATAC TTTCAGACAA ACAGAAAAAA AAA	2153

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met His Leu Thr Val Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp
-316 -315 -310 -305

Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn
-300 -295 -290 -285

His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg
-280 -275 -270

Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
-265 -260 -255

Pro Arg Pro Phe Ser Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala
-250 -245 -240

Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu
-235 -230 -225

Ser Glu Tyr Ser Val Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala
-220 -215 -210 -205

Arg Lys Gly Tyr Pro Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln
-200 -195 -190

Leu Ser Arg Thr Thr Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser
-185 -180 -175

Leu His Asp Thr Asn Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe
-170 -165 -160

Val Asn Leu Val Glu Arg Asp Lys Asp Phe Ser His Gln Arg Arg His
-155 -150 -145

Tyr Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala
-140 -135 -130 -125

Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg
-120 -115 -110

Phe Glu Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu
-105 -100 -95

Tyr Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala
-90 -85 -80

Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser
-75 -70 -65

Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys
-60 -55 -50 -45

Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu
-40 -35 -30

Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe
-25 -20 -15

Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys
-10 -5 1

Arg Lys Asn Gln Asn Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser
5 10 15 20

Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala
25 30 35

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
40 45 50

Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
55 60 65

Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
70 75 80

Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
85 90 95 100

Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
105 110 115

Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
120 125 130

Arg Ser Cys Gly Cys His
135

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Human Heart

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human heart cDNA library stratagene catalog #936208
- (B) CLONE: hH38

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..850

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 427..843

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 1..997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC 49
Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile
-139 -135 -130

CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG 97
Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val
-125 -120 -115 -110

CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG 145
Pro Ser Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln

	-105	-100	-95	
GTG GTC CAG GAG CAG TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT Val Val Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp				193
-90 -85 -80				
CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val				241
-75 -70 -65				
ACA GCA GCC AGT GAC TGC TGG CTG AAG CGT CAC AAG GAC CTG GGA Thr Ala Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly				289
-60 -55 -50				
CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC GTG GAT CCT GGC Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly				337
-45 -40 -35 -30				
CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe				385
-25 -20 -15				
GTC GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg				433
-10 -5 1				
GCA GTG AGG CCA CTG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG Ala Val Arg Pro Leu Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu				481
5 10 15				
CCG CAG GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser				529
20 25 30 35				
CAC GGC CGG CAG GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln				577
40 45 50				
GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala				625
55 60 65				
TAT TAC TGT GAG GGG GAG TGC TCC TTC CCG CTG GAC TCC TGC ATG AAC Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn				673
70 75 80				
GCC ACC AAC CAC GCC ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro				721
85 90 95				
AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr				769
100 105 110 115				
TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His				817
120 125 130				
CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCC CGCCCCAGCCCC Arg Asn Met Val Val Lys Ala Cys Gly Cys His				870

930

990

1003

TAATGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC
 TGTCACAGCT CAAGCAGGAG TGTCAAGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG
 CTTCTGGAA TTC

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
 -139 -135 -130 -125

Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser
 -120 -115 -110

Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val
 -105 -100 -95

Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
 -90 -85 -80

Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala
 -75 -70 -65 -60

Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg
 -55 -50 -45

Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala
 -40 -35 -30

Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
 -25 -20 -15

Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val
 -10 -5 1 5

Arg Pro Leu Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
 10 15 20

Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly
 25 30 35

Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu
 40 45 50

Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr
 55 60 65

Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr

70

75

80

85

Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala
 90 95 100

Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
 105 110 115

Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
 120 125 130

Met Val Val Lys Ala Cys Gly Cys His
 135 140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pALBP2-781

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2724..3071

(ix) FEATURE:

- (A) NAME/KEY: terminator
- (B) LOCATION: 3150..3218

(ix) FEATURE:

- (A) NAME/KEY: RBS
- (B) LOCATION: 2222..2723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACGAAAGGG CCTCGTGATA CGCCTATTAA TATAGGTAA TGTCATGATA ATAATGGTTT	60
CTTAGACGTC AGGTGGCACT TTTGGGAA ATGTGCCGG AACCCCTATT TGTTTATTAA	120
TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT	180
AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTT	240
TTGCAGCATT TTGCCTTCCT GTTTTGCTC ACCCAGAAC GCTGGTGAAA GTAAAAGATG	300
CTGAAGATCA GTGGGTGCA CGAGTGGTT ACATCGAAC GGATCTAAC AGCGGTAAGA	360
TCCTTGAGAG TTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC	420
TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC	480
ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG	540

GCATGACAGT AAGAGAATT A TCCAGTGCT G CCATAACC AT GAGTGATAAC ACTGCGGCC A	600
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTG CACAACATGG	660
GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG	720
ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAA AC GTTGC GCAAA CTATTAAC TG	780
GCGAACTACT TACTCTAGCT TCCCCGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG	840
TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAACTG	900
GAGCCGGTGA CGGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT	960
CCCGTATCGT AGTTATCTAC ACGACGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC	1020
AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTACT	1080
CATATATACT TTAGATTGAT TTAAAACCTTC ATTTTAATT TAAAAGGATC TAGGTGAAGA	1140
TCCTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTCGTTC CACTGAGCGT	1200
CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTCTG CGCGTAATCT	1260
GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTGCCG GATCAAGAGC	1320
TACCAACTCT TTTTCCGAAG GTA ACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC	1380
TTCTAGTGT A GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC	1440
TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG	1500
GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT	1560
CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGT	1620
AGCATTGAGA AAGCGCCACCG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG	1680
GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTT	1740
ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGTA TGCTCGTCAG	1800
GGGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTT	1860
GCTGGCCTTT TGCTCACATG TTCTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA	1920
TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT	1980
CAGTGAGCGA GGAAGCGGAA GAGCGCCAA TACGCAAACCA GCCTCTCCCC GCGCGTTGGC	2040
CGATTCAATTA ATGCAGAATT GATCTCTCAC CTACCAAACA ATGCCCCCT GCAAAAAATA	2100
AATTCAATATA AAAAACATAC AGATAACC AT CTGCGGTGAT AAATTATCTC TGGCGGTGTT	2160
GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGGACTG ACCACCATGA	2220
AGGTGACGCT CTTAAAATT AAGCCCTGAA GAAGGGCAGC ATTCAAAGCA GAAGGCTTTG	2280
GGGTGTGTGA TACGAAACGA AGCATTGGCC G TAAAGTGGGA TTCCGGATTA GCTGCCAATG	2340

TGCCAATCGC GGGGGGTTT CGTCAGGAC TACAAC TGCC ACACACC ACC AAAGCTAACT	2400
GACAGGAGAA TCCAGATGGA TGCACAAACA CGCCGCCGCG AACGTGCGC AGAGAAACAG	2460
GCTCAATGGA AAGCAGCAA TCCCCTGTTG GTTGGGTAA GCGAAAACC AGTTCCGAAA	2520
GATTTTTTA ACTATAAACG CTGATGGAAG CGTTTATGCG GAAGAGGTAA AGCCCTCCC	2580
GAGTAACAAA AAAACAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA	2640
GGGCATCAAA TTAAACCACA CCTATGGTGT ATGCATTAT TTGCATACAT TCAATCAATT	2700
GTTATCTAAG GAAATACTTA CAT ATG CAA GCT AAA CAT AAA CAA CGT AAA Met Gln Ala Lys His Lys Gln Arg Lys	2750
1 5	
CGT CTG AAA TCT AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC AGT Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser	2798
10 15 20 25	
GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala	2846
30 35 40	
TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn	2894
45 50 55	
TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser	2942
60 65 70	
AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser	2990
75 80 85	
ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln	3038
90 95 100 105	
GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA Asp Met Val Val Glu Gly Cys Gly Cys Arg	3088
110 115	
CATAAAATATA TATATATATA TATATTTAG AAAAAAGAAA AAAATCTAGA GTCGACCTGC	3148
AGTAATCGTA CAGGGTAGTA CAAATAAAA AGGCACGTCA GATGACGTGC CTTTTTCTT	3208
GTGAGCAGTA AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCTGG	3268
CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA	3328
AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCAGCAGC CTGAATGGCG AATGGCCCT	3388
GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTCA CACCGCATAT ATGGTGCACT	3448
CTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC	3508
GCTGACCGCGC CCTGACGGGC TTGTCTGCTC CGGGCATCCG CTTACAGACA AGCTGTGACC	3568

GTCTCCGGGA GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGA

3623

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys
1 5 10 15

Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp
20 25 30

Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys
35 40 45

Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val
50 55 60

Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
65 70 75 80

Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn
85 90 95

Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys
100 105 110

Gly Cys Arg
115

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATGGGCAGC TGAG

14

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGGTTGTG GGTGTCGCTA GTGAGTCGAC TACAGCAAAT T

41

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATGTGGGT GCCGCTGACT CTAGAGTCGA CGGAATTG

38

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCACCAT GATTCTGGT AACCGAATGC T

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGGTACTAA GGACCATTGG CTTAC

25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGACCTGCAG CCATGCATCT GACTGTA

27

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGCCTGCAGT TTAATATTAG TGGCAGC

27

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGACCTGCAG CCACC

15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCGACCCACC ATGCCGGGGC TGGGGCGGAG GGCGCAGTGG CTGTGCTGGT GGTGGGGCT 60

GTGCTGCAGC TGCTGCGGGC C 81

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAGCAGCT GCACAGCAGC CCCCACCACC AGCACAGCCA CTGCGCCCTC CGCCCCAGCC 60

CCGGCATGGT GGG 73

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCGACTGGTT T 11

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGAAACCAG 9

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGACAGGCT CGCCTGCA

18

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCCGAGCGG

10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTGACC CACCATGCAC GTGCGCTCA

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCTGTGACC TCGGAGGAGC TAGTGGC

27

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: bmp-3

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 321..1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATCTTGAA AACACCCGGG CCACACACGC CGCGACCTAC AGCTCTTCT CAGCGTTGGA	60
GTGGAGACGG CGCCCGCAGC GCCCTGCGCG GGTGAGGTCC GCGCAGCTGC TGGGAAAGAG	120
CCCACCTGTC AGGCTGCGCT GGGTCAGCGC AGCAAGTGGG GCTGGCCGCT ATCTCGCTGC	180
ACCCGGCCGC GTCCCGGGCT CCGTGCAGCC TCGCCCCAGC TGGTTGGAG TTCAACCCTC	240
GGCTCCGCCG CCGGCTCCTT GCGCCTTCGG AGTGTCCCGC AGCGACGCCG GGAGCCGACG	300
CGCCGGCGCG GTACCTAGCC ATG GCT GGG GCG AGC AGG CTG CTC TTT CTG Met Ala Gly Ala Ser Arg Leu Leu Phe Leu 1 5 10	350
TGG CTG GGC TGC TTC TGC GTG AGC CTG GCG CAG GGA GAG AGA CCG AAG Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys 15 20 25	398
CCA CCT TTC CCG GAG CTC CGC AAA GCT GTG CCA GGT GAC CGC ACG GCA Pro Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala 30 35 40	446
GGT GGT GGC CCG GAC TCC GAG CTG CAG CCG CAA GAC AAG GTC TCT GAA Gly Gly Pro Asp Ser Glu Leu Gln Pro Gln Asp Lys Val Ser Glu 45 50 55	494
CAC ATG CTG CGG CTC TAT GAC AGG TAC AGC ACG GTC CAG GCG GCC CGG His Met Leu Arg Leu Tyr Asp Arg Tyr Ser Thr Val Gln Ala Ala Arg 60 65 70	542
ACA CCG GGC TCC CTG GAG GGA GGC TCG CAG CCC TGG CGC CCT CGG CTC Thr Pro Gly Ser Leu Glu Gly Ser Gln Pro Trp Arg Pro Arg Leu 75 80 85 90	590
CTG CGC GAA GGC AAC ACG GTT CGC AGC TTT CGG GCG GCA GCA GAA Leu Arg Glu Gly Asn Thr Val Arg Ser Phe Arg Ala Ala Ala Glu 95 100 105	638
ACT CTT GAA AGA AAA GGA CTG TAT ATC TTC AAT CTG ACA TCG CTA ACC Thr Leu Glu Arg Lys Gly Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr 110 115 120	686

AAG TCT GAA AAC ATT TTG TCT GCC ACA CTG TAT TTC TGT ATT GGA GAG Lys Ser Glu Asn Ile Leu Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu 125 130 135	734
CTA GGA AAC ATC AGC CTG AGT TGT CCA GTG TCT GGA GGA TGC TCC CAT Leu Gly Asn Ile Ser Leu Ser Cys Pro Val Ser Gly Gly Cys Ser His 140 145 150	782
CAT GCT CAG AGG AAA CAC ATT CAG ATT GAT CTT TCT GCA TGG ACC CTC His Ala Gln Arg Lys His Ile Gln Ile Asp Leu Ser Ala Trp Thr Leu 155 160 165 170	830
AAA TTC AGC AGA AAC CAA AGT CAA CTC CTT GGC CAT CTG TCA GTG GAT Lys Phe Ser Arg Asn Gln Ser Gln Leu Leu Gly His Leu Ser Val Asp 175 180 185	878
ATG GCC AAA TCT CAT CGA GAT ATT ATG TCC TGG CTG TCT AAA GAT ATC Met Ala Lys Ser His Arg Asp Ile Met Ser Trp Leu Ser Lys Asp Ile 190 195 200	926
ACT CAA TTC TTG AGG AAG GCC AAA GAA AAT GAA GAG TTC CTC ATA GGA Thr Gln Phe Leu Arg Lys Ala Lys Glu Asn Glu Glu Phe Leu Ile Gly 205 210 215	974
TTT AAC ATT ACG TCC AAG GGA CGC CAG CTG CCA AAG AGG AGG TTA CCT Phe Asn Ile Thr Ser Lys Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro 220 225 230	1022
TTT CCA GAG CCT TAT ATC TTG GTA TAT GCC AAT GAT GCC GCC ATT TCT Phe Pro Glu Pro Tyr Ile Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser 235 240 245 250	1070
GAG CCA GAA AGT GTG GTA TCA AGC TTA CAG GGA CAC CGG AAT TTT CCC Glu Pro Glu Ser Val Val Ser Ser Leu Gln Gly His Arg Asn Phe Pro 255 260 265	1118
ACT GGA ACT GTT CCC AAA TGGGATAGCC ACATCAGAGC TGCCCTTTCC Thr Gly Thr Val Pro Lys 270	1166
ATTGAGCGGA GGAAGAACCG CTCTACTGGG GTCTTGCTGC CTCTGCAGAA CAACGAGCTT	1226
CCTGGGGCAG AATACCAGTA TAAAAAGGAT GAGGTGTGGG AGGAGAGAAA GCCTTACAAG	1286
ACCCTTCAGG CTCAGGCCCT TGAAAAGAGT AAGAATAAAA AGAACACAGAG AAAGGGCCT	1346
CATCGGAAGA GCCAGACGCT CCAATTGAT GAGCAGACCC TGAAAAGGC AAGGAGAAAG	1406
CAGTGGATTG AACCTCGGAA TTGCGCCAGG AGATACCTCA AGGTAGACTT TGCAGATATT	1466
GGCTGGAGTG AATGGATTAT CTCCCCAAG TCCTTGATG CCTATTATTG CTCTGGAGCA	1526
TGCCAGTTCC CCATGCCAAA GTCTTGAAG CCATCAAATC ATGCTACCAT CCAGAGTATA	1586
GTGAGAGCTG TGGGGTCGT TCCTGGATT CCTGAGCCTT GCTGTGTACC AGAAAAGATG	1646
TCCTCACTCA GTATTTATT CTTGATGAA AATAAGAATG TAGTGCTTAA AGTATACCCCT	1706
AACATGACAG TAGAGTCTTG CGCTTGCAGA TAACCTGGCA AAGAACTCAT TTGAATGCTT	1766

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Gly Ala Ser Arg Leu Leu Phe Leu Trp Leu Gly Cys Phe Cys
1 5 10 15

Val Ser Leu Ala Gln Gly Glu Arg Pro Lys Pro Pro Phe Pro Glu Leu
20 25 30

Arg Lys Ala Val Pro Gly Asp Arg Thr Ala Gly Gly Pro Asp Ser
35 40 45

Glu Leu Gln Pro Gln Asp Lys Val Ser Glu His Met Leu Arg Leu Tyr
50 55 60

Asp Arg Tyr Ser Thr Val Gln Ala Ala Arg Thr Pro Gly Ser Leu Glu
65 70 75 80

Gly Gly Ser Gln Pro Trp Arg Pro Arg Leu Leu Arg Glu Gly Asn Thr
85 90 95

Val Arg Ser Phe Arg Ala Ala Ala Glu Thr Leu Glu Arg Lys Gly
100 105 110

Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr Lys Ser Glu Asn Ile Leu
115 120 125

Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu Leu Gly Asn Ile Ser Leu
130 135 140

Ser Cys Pro Val Ser Gly Gly Cys Ser His His Ala Gln Arg Lys His
145 150 155 160

Ile Gln Ile Asp Leu Ser Ala Trp Thr Leu Lys Phe Ser Arg Asn Gln
165 170 175

Ser Gln Leu Leu Gly His Leu Ser Val Asp Met Ala Lys Ser His Arg
180 185 190

Asp Ile Met Ser Trp Leu Ser Lys Asp Ile Thr Gln Phe Leu Arg Lys
195 200 205

Ala Lys Glu Asn Glu Glu Phe Leu Ile Gly Phe Asn Ile Thr Ser Lys
210 215 220

Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro Phe Pro Glu Pro Tyr Ile
225 230 235 240

Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser Glu Pro Glu Ser Val Val
245 250 255

Ser Ser Leu Gln Gly His Arg Asn Phe Pro Thr Gly Thr Val Pro Lys
260 265 270

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTCTCATA ATCGTTCTAA AACTCCAAAA AATCAAGAAG CTCTGCGTAT GGCCAACGTG	60
GCAGAGAACCA GCAGCAGCGA CCAGAGGCAG GCCTGTAAGA AGCACGAGCT GTATGTCAGC	120
TTCCGAGACC TGGGCTGGCA GGACTGGATC ATCGGCCCTG AAGGCTACGC CGCCTACTAC	180
TGTGAGGGGG AGTGTGCCTT CCCTCTGAAC TCCTACATGA ACGCCACCAA CCACGCCATC	240
GTGCAGACGC TGGTCCACTT CATCAACCCG GAAACGGTGC CCAAGCCCTG CTGTGGCCCC	300
ACGCAGCTCA ATGCCATCTC CGTCCTCTAC TTGATGACA GCTCCAACGT CATCCTGAAG	360
AAATACAGAA ACATGGTGGT CCGGCCGT GGCTGCCACT AGCTCCTCCG AGAATTCAAGA	420
CCCTTGGGG CCAAGTTTT CTGGATCCT	449

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAAGAAGGAG ATATACAT	18
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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGCGTAAAC AATGGATTGA ACCACGTAAC TGTGCTCGTC GTTATCTGAA AGTAGACTTT	60
GCAGATATTG GCTGGAGTGA ATGGATTATC TCCCCAAGT CCTTGATGC CTATTATTGC	120
TCTGGAGCAT GCCAGTTCCC CATGCCAAAG TCTTGAAAGC CATCAAATCA TGCTACCATC	180
CAGAGTATAG TGAGAGCTGT GGGGGTCGTT CCTGGGATTC CTGAGCCTTG CTGTGTACCA	240
GAAAAGATGT CCTCACTCAG TATTTTATTC TTTGATGAAA ATAAGAATGT AGTGCTTAAA	300
GTATAACCCTA ACATGACAGT AGAGTCTTGC GCTTGCAGAT AACCTGGCAA AGAACTCATT	360
TGAATGCTTA ATTCAAT	377